

AMENDMENTS TO THE SPECIFICATION

Please replace the 3rd paragraph on page 8 with the following amended paragraph:

Calculation of maximum ~~[[%]]~~percent homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the GCG Wisconsin Bestfit package (University of Wisconsin, U.S.A.; Devereux *et al.*, 1984, Nucleic Acids Research 12:387). Examples of other software ~~[[than]]~~ that can perform sequence comparisons include, but are not limited to, the BLAST package (~~see <http://www.ncbi.nih.gov/BLAST/>~~), FASTA (Atschul *et al.*, 1990, J. Mol. Biol., 403-410; FASTA is also available ~~[[for]]~~ online ~~searching at, for example,~~ ~~<http://www2.ebi.ac.uk/fasta3>~~) and the GENEWORKS suite of comparison tools. However, it is preferred to use the GCG Bestfit program.